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Research Article

Performance of Brinjal (Solanum melongena) Genotypes through Genetic Variability Analysis

Most. Nur Shahi Begum[1], Bir Jahangir Shirazy[2]*, Md. Mostofa Mahbub[3], and Md. Ashaduzzaman Siddikee[4]

[1] Department of Genetics and Plant Breeding, Sher-e-Bangla Agriculture University, Dhaka, Bangladesh

[2] Scientific Officer, Rice Farming Systems Division, Bangladesh Rice Research Institute (BRRI), Gazipur, Bangladesh

[3] Scientific Officer, Agronomy Division, BRRI, Gazipur, Bangladesh

[4] Associate Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agriculture University, Dhaka, Bangladesh

Abstract:

The physiomorphological divergence was assessed in fifteen brinjal genotypes by using cluster mean analysis and mean difference to identify parental genotypes for future breeding program in order to develop new high yielding varieties in randomized complete block design with three replications. Plant height, days to first flowering, number of branch and number of fruits per plant have the highest percent of variations among the traits. The genotypes under the experiment were grouped into five clusters. The highest inter cluster distance was found between cluster III and IV followed by IV and V. According to relative contributions of the nine characters length of fruit and yield per plant have the prominent influence towards varietal improvement. Selecting genotypes from distant clusters probably provide promising recombinants and better segregants for future breeding platform.

Keywords: Cluster; clusters mean; genotype; genetic variation

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***Correspondence to:** Bir Jahangir Shirazy, Scientific Officer, Rice Farming Systems Division, BRRI, Gazipur, Bangladesh

Email: bjshirazy@yahoo.com

1. Introduction

Eggplant (*Solanum melongena* L), is a member of the family Solanaceae. It is widely cultivated as vegetable in both temperate and tropical areas, especially in Asia. Brinjal (*Solanum melongena*) is one of the important vegetable crops grown in all parts of Bangladesh. It has a positive role in both summer and winter to fulfill the market demand of vegetables of Bangladesh. Yield potentiality of the varieties cultivated in Bangladesh is less and brinjal size, shape, skin colour varies in different locations. Improvement in fruit yield, colour, and insect resistances. The current nutritional condition of third world and some emerging countries like Bangladesh is a matter of great fear since the most of the public's are suffering from malnutrition [1-3]. Brinjal can show a significant role in this case and can aid to meet up the nutritional shortage difficulty. Considering the potentiality of this crop, there is a need for improvement and to develop varieties suited to specific agro-ecological conditions and also for specific end use. Due to low soil fertility and stress condition [4] yield of Brinjal is poor in Bangladesh. Genetic diversity is a major factor that determines prospects of yield improvement in future. Knowledge of genetic diversity within a crop and correlation among the yield contributing characters is essential for the long-term success of a breeding program and maximizes the exploration of germplasm resources [1]. Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm. Multivariate analysis acts as a useful tool to quantify the degree of divergence between the biological populations at genotypic level and to assess the relative contribution of different components to the total divergence both inter and intra cluster levels [4,5]. The present study was undertaken to estimate the nature and magnitude of genetic diversity of brinjal and the feasibility of utilizing all those information for the varietal improvement of the brinjal.

2. Materials and Method

The experiment was carried out to evaluate the genetic diversity, correlation and path coefficient analysis between fifteen brinjal genotypes (Table 1) during November, 2013 to April, 2014 at the research field of Sher-e-Bangla Agricultural University, located at 23° 77′ N latitude, 90° 33′ E longitude at an altitude of 8.6 m above sea level in Dhaka, Bangladesh. Fifteen brinjal genotypes were sown in randomized complete block design with three replications; every plot lied of a single row of 5m long with row to row space of 1m preserving 2 plants per meter. Data were collected from ten randomly selected plants.

Statistical Analysis

The data were analyzed by MSTAT program for ANOVA and analyzed by Mahalanobi's D2 statistics, principal component analysis, cluster mean analysis, principal coordinate analysis (PCA) and canonical variate analysis (CVA). Fifteen brinjal genotypes were grouped into cluster by using Genstat v 5.5 software.

3. Results and Discussion

Performance of Different Traits

Means regarding different plant traits and their comparison are given in Table 2. The present result revealed that height of plant was highly significant affected due to various brinjal genotypes. The plant

height ranged from 47.33 to 71.33 cm. The line BD-2705 was found lowest plant height, whereas genotype Sada begun had highest plant height. BD-2750, BD-2704, Sada begun and BD-2724 showed the early flowering and Uttorahajari showed the late flowering. The number of branches is the most important yield component in soybean. The effective and fruit bearing branches play important role in enhancing the final yield. The number of branches varies from genotype to genotype depending upon genetic potential of a variety. In present study the number of branches was significantly affected by the various genotypes. The highest branches (8.00) were produced by Uttorahajari and BD-2662 followed by BD-2724 (6.67) and BD-2754 (6.33). Similarly BD-2796 and BD-2698 had shown very poor performance by showing only 2.67 and 3.33, branches per plant respectively. Highest fruit bearing genotype was BD-2791. Highest fruit diameter (20.03 cm) found in Sada begun. Fruit weight is an important yield parameter and is vary from genotype to genotype. BD-2724 genotype showed the highest fruit weight (111.80 g). BD-2791 genotype has showed the maximum yield per plant. May be due to early flowering Uttorahajari have the highest insect infestation.

Eigen Values

The principle component analysis yielded four of the eigen values above unity accounted for 80.94% of the total variation and the last five principle accounted for near about 20% of the total variation (Table 3).

Cluster Analysis

The distribution pattern in table 4 indicated that the maximal number of genotypes (7) was comprised in cluster I followed by cluster II (4), cluster IV (2), cluster III (1) and cluster V (1). Mahbub et al., 2016 also grouped the soybean genotypes into different clusters and found different number of genotypes in different cluster.

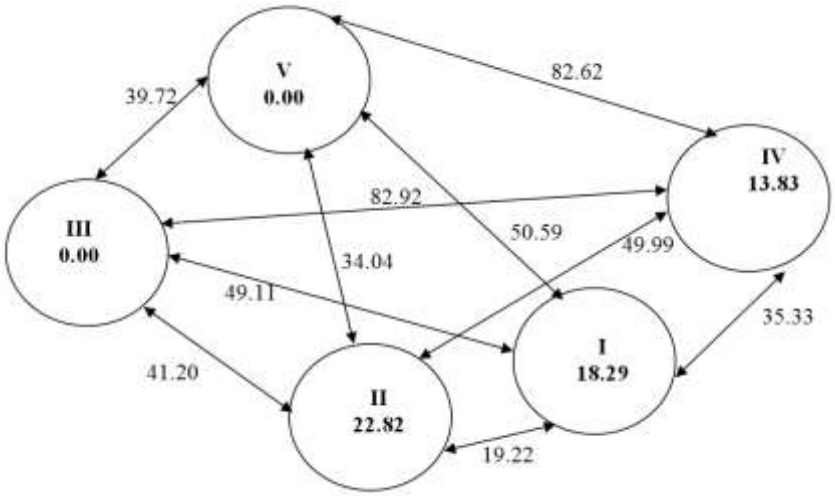

Figure 1 Diagram showing inter-cluster (outside the circle) and intra-cluster (inside the circle) distances of fifteen genotypes of brinjal

There was much variation among the clusters compared to intra-cluster variations (Table 5 and Figure 1). The highest intra-cluster distance was observed in cluster II (22.82) and the lowest in cluster II (0.000). The inter-cluster distance was maximum between cluster III and IV (82.92) followed by cluster IV and V (82.62); cluster I and V (50.59) and cluster II and IV (49.99) suggesting that the genotypic materials

belonging to these clusters may be used as parents for hybridization programme to develop desirable variety because crosses between genetically divergent lines will generate heterotic segregants [6,7].

From Table 6 it was observed that G6 and G14 have highest inter genotypic distance whereas G3 and G6 have the lowest distance. We know that heterosis can be best exploited and chances of getting transgressive segregants are maximum when generating diverse lines are crossed. Because the genotypes from diverge cluster may be advised for inclusion in hybridization program as they are expected to develop excellent segregants [4,8].

Table 1 Characterization of fifteen brinjal genotypes

Genotype No.	Name of the genotypes	Growth Habit	Hairiness	Fruit shape	Fruit color	Spiny character
G1	Bolaka green	Erect	Leaf, Stem	Round	Whitish green	Fruit stock
G2	BD-2698	Semi erect	Leaf, Stem	Ovate	Whitish green	Stem, Fruit stock
G3	BD-2754	Semi erect	Leaf, Stem	Round	Whitish green	Stem, Fruit stock
G4	BD-2705	Spreading	Leaf, Stem	Ovate	Purplish green	Stem, Fruit stock
G5	BD-2775	Semi erect	Leaf, Stem	Round	Purplish green	Stem, Fruit stock
G6	BD-2791	Spreading	Leaf, Stem	Ovate	Whitish green	Stem
G7	BD-2796	Erect	Leaf, Stem	Round	Whitish green	Stem, Fruit stock
G8	Uttora hajari	Spreading	Leaf, Stem	Ovate	Violet	Fruit stock
G9	BD-2750	Spreading	Leaf, Stem	Round	Whitish green	Stem, Sepal
G10	BD-2662	Spreading	Leaf, Stem	Round	Violet	Fruit stock
G11	Plastid black beauty	Semi erect	Leaf, Stem	Round	violet	Stem, Fruit stock
G12	BD-2704	Erect	Leaf, Stem	ovate	purple	Fruit stock
G13	Sada begun	Erect	Leaf, Stem	ovate	White	Stem
G14	BD-2653	Erect	Leaf, Stem	long	Whitish purple	Fruit stock
G15	BD-2724	Semi erect	Leaf, Stem	Round	Whitish purple	Fruit stock

Table 2 Mean performance of nine characters of fifteen brinjal genotypes

	Genotypes	Plant height (cm)	Days of 1st flowering	Number of branch	Number of fruits per plant	Diameter of the fruit (cm)	Length of the fruit (cm)	Weight per fruit (g)	Yield per plant (kg)	% insect infestation
1	Bolaka green	71.00 a	61.00 e	5.00cde	24.00 cd	16.67 c	7.90bc	63.37 h	1.52 c	27.23 b
2	BD-2698	69.67 ab	62.00 de	3.33fg	17.67fg	18.70abc	8.03 b	78.93 e	1.39 d	15.47ef
3	BD-2754	64.33 c	64.67 cd	6.33bc	10.67 i	14.50 d	8.17 b	88.97 d	0.95 g	24.73bc
4	BD-2705	47.33 f	65.00 cd	3.33fg	12.00 hi	17.67bc	11.00 a	98.37 c	1.17 e	23.80bc
5	BD-2775	70.33 a	65.67 cd	4.33def	20.00 def	13.33 de	5.00ef	69.97 f	1.39 d	19.23 de
6	BD-2791	53.00 e	65.00 cd	4.67def	**45.67 a**	11.33ef	8.17 b	60.93 h	**2.78 a**	**19.37 de**
7	BD-2796	58.33 d	66.33 c	2.67g	15.33gh	17.93abc	8.33 b	61.63 h	0.94 g	18.60 de
8	Uttorahajari	64.33 c	82.33 a	8.00 a	**3.00 j**	19.20ab	6.33cde	102.20 b	0.31 i	36.63 a
9	BD-2750	65.67 bc	54.00 f	4.00efg	17.67efg	17.33bc	8.17 b	62.37 h	1.11 f	25.73bc
10	BD-2662	57.67 d	62.33 de	8.00 a	28.00 b	12.87 def	4.67 f	20.30 j	0.56 h	18.73 de
11	Plastid black beauty	57.67 d	60.33 e	5.00cde	15.67gh	16.77 c	5.67 def	89.80 d	1.40 d	22.83 cd
12	BD-2704	66.00 bc	55.00 f	4.33 def	22.67 d	10.77 f	7.17bcd	66.51 g	1.50 c	13.60 f
13	Sada begun	71.33 a	52.67 f	5.67bcd	27.67bc	20.03 a	8.00bc	39.87 i	1.10 f	12.93 f
14	BD-2653	66.33 bc	71.33 b	5.67bcd	16.67fg	11.10 f	11.00 a	15.57 k	0.23 j	16.93ef
15	BD-2724	55.33 de	55.67 f	6.67ab	21.67 de	14.50 d	7.67bc	**111.80 a**	**2.42 b**	18.90 de
	CV (%)	3.57	3.18	14.97	11.19	7.76	11.75	2.48	1.71	11.14
	LSD (0.05)	**3.74**	**3.34**	**1.29**	**3.72**	**2.01**	**1.51**	**2.85**	**0.04**	**3.91**

Table 3 Eigen values and yield percent contribution of nine characters of fifteen brinjal genotypes

Characters	Eigen values	Percent variation	Cumulative % of percent variation
Plant height (cm)	2.82	31.32	31.32
Days of 1st flowering	1.78	19.80	51.12
Number of branch	1.48	16.42	67.54
Number of fruits per plant	1.21	13.40	80.94
Diameter of the fruit (cm)	0.54	6.03	86.97
Length of the fruit (cm)	0.48	5.35	92.33
Weight per fruit (g)	0.44	4.87	97.20
Yield per plant (kg)	0.24	2.70	99.90

Table 4 Distribution of fifteen brinjal genotypes in five different clusters

Cluster No.	Number of populations	Name of genotypes
I	7	Bolaka green, BD-2698, BD-2775, BD-2796, BD-2750, Plastic Black Beauty, BD-2653
II	4	BD-2754, BD-2705,**BD-2791**, BD-2704
III	1	Uttorahajari
IV	2	BD-2662, Sada begun
V	1	BD-2724

Table 5 Intra (bold) and inter cluster distances (D^2) for 27 genotypes of brinjal

	I	II	III	IV	V
I	18.29				
II	19.22	22.82			
III	49.11	41.20	0.00		
IV	35.33	49.99	82.92	13.83	
V	50.59	34.04	39.72	82.62	0.00

Table 6 Inter-genotypic distance (D^2) of different genotypes

Between genotypes	Distance(D^2)	Between genotypes	Distance(D^2)
G1-G4	4.72	G6-G15	4.91
G1-G10	4.74	G7-G8	4.58
G2-G10	4.91	G7-G12	4.61
G3-G6	4.51	G7-G15	4.67
G4-G5	4.97	G8-G9	4.85
G4-G8	4.54	G8-G10	4.63
G4-G10	4.89	G8-G12	5.11
G4-G13	4.75	G8-G13	4.87
G4-G14	4.93	G8-G14	5.02
G4-G15	4.94	G8-G15	5.08
G5-G13	4.77	G9-G14	4.72
G5-G14	4.54	G9-G14	4.80
G5-G15	4.67	G10-G14	4.77
G6-G7	4.59	G10-G15	5.06
G6-G8	5.01	G11-G14	4.76
G6-G9	4.94	G12-G14	4.66
G6-G10	4.73	G12-G15	4.76
G6-G12	4.60	G13-G14	5.01
G6-G13	4.97	G13-G15	4.82
G6-G14	5.13	G14-G15	4.93

Table 7 Cluster mean for 9 characters of 15 genotypes of eggplant

Class	Plant height (cm)	Branch per plant (no.)	Fruits per plant (no.)	Fruit diameter (cm)	Length of fruit (cm)	Days to first flower	Yield per plant (kg)	Fruit weight (g)	% insect infes-tation
I	65.57	4.29	18.14	15.98	7.73	62.95	1.14	63.09	20.86
II	57.67	4.67	22.75	13.57	8.63	62.42	1.60	78.70	20.38
III	64.33	8.00	3.00	19.20	6.33	82.33	0.31	102.20	36.63
IV	64.50	6.83	27.83	16.45	6.33	57.50	0.83	30.08	15.83
V	55.33	6.67	21.67	14.50	7.67	55.67	2.42	111.83	18.90

Table 8 Relative contributions of the nine characters of fifteen genotypes to the total divergence

Parameter	Vector 1	Vector 2
Plant height (cm)	-0.032	-0.428
Branch per plant	-0.199	-0.357
Fruits per plant	0.510	-0.060
Fruit diameter (cm)	-0.299	0.228
Length of fruit (cm)	0.022	0.231
Days to first flower	-0.417	-0.111
Yield per plant (kg)	0.380	0.447
Fruit weight (g)	-0.238	0.591
% insect infestation	-0.483	0.137

Cluster Means for the Characters

Intra-cluster mean for nine physiological characters are present in Table 7. It was perceived that cluster III showed the maximum value for number of branches per plant, Fruit diameter and percent insect infes-tation. Yield per plant, Fruit weight have higher value in cluster V; Plant height in cluster I; Length of fruit in cluster II and Fruits per plant in cluster IV. Cluster V also suited for early flowering which is also very much desirable. Among these clusters, the cluster III and V showed the maximum desirable traits which could be reflected in the assortment of parents for future breeding program. The genotypic materials from these clusters could be used for breeding purpose in crop improvement project [5,9].

Contribution of Traits Towards Diversity

The characters having greater contribution to the total divergence were given highest emphasis for grouping on the cluster for hybridization. Contribution of characters towards divergence obtain from CVA is presented in Table 8, where the values of vector-1 and 2 transpired that contribution of length of fruit and yield per plant were found prominent to the total divergence. In vector-1, the other important traits responsible for differentiation were fruits per plant while in vector-2, fruit diameter, fruit weight and insect infestation was important. Insect infestation and days to first flowering has highly negative relation with vector-1 and plant height with vector-2. Interesting fruits per plant, fruit diameter, fruit weight and insect infestation have negative relation with one vector but positive relation with opposite vector. So during selection program these characters should be under consider for breeding program.

4. Conclusion

Based on the results of this experiment, it may be concluded that breeding program should be undertaken by picking as parental genotypes from diverse distant clusters along with considering the cluster mean values of different traits for find the desirable characters which have active relative contribution to the total divergence aimed at developing anticipated varieties by selection of superior genotypes through the successive positive principal coordinate and canonical variants involvement generations.

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